

## In the Claims

C2  
Claim 33 (amended) A method for obtaining one or more candidate nucleotide sequences, the candidate nucleotide sequences being indicative of a sequence of a target polynucleotide molecule T, T producing a hybridization signal  $I(\bar{x})$  upon incubating T with a polynucleotide  $\bar{x}$  for each polynucleotide  $\bar{x}$  in a set E of polynucleotides, the method comprising the steps of:

- (a) for each polynucleotide  $\bar{x}$  in the set E of polynucleotides, obtaining a probability  $P_0(\bar{x})$  of the hybridization signal  $I(\bar{x})$  when the sequence  $\bar{x}$  is not complementary to a subsequence of T and a probability  $P_1(\bar{x})$  of the hybridization signal when the sequence  $\bar{x}$  is complementary to a subsequence of T; so as to obtain a probabilistic spectrum (PS) of T;
- (b) assigning a score to each of a plurality of candidate nucleotide sequences, the score being obtained in a calculation using the probabilistic spectrum and at least one reference nucleotide sequence H, the score being indicative of the candidate nucleotide sequence being a variant of H and furthermore being indicative of the probability that the candidate would give rise to the hybridization signal  $I(\bar{x})$ ; and
- (c) selecting one or more candidate nucleotide sequences having an essentially maximal score.

C3  
Claim 54 (amended) The method according to claim 33 wherein the target comprises two or more polynucleotide molecules.

C4  
Claim 63 (amended) A program storage device readable by machine, tangibly embodying a program of instructions executable by the machine to perform method steps for obtaining a candidate nucleotide sequence, the candidate nucleotide sequence being indicative of a sequence of a target polynucleotide molecule T, T

producing a hybridization signal  $I(\bar{x})$  upon incubating T with a polynucleotide  $\bar{x}$  for each polynucleotide  $\bar{x}$  in a set E of polynucleotides, the method comprising the steps of:

- (a) for each polynucleotide  $\bar{x}$  in the set E of polynucleotides, obtaining a probability  $P_0(\bar{x})$  of  $I(\bar{x})$  when the sequence  $\bar{x}$  is not complementary to a subsequence of T and a probability  $P_1(\bar{x})$  of  $I(\bar{x})$  when the sequence  $\bar{x}$  is complementary to a subsequence of T; so as to obtain a probabilistic spectrum (PS) of T;
- (b) assigning a score to each of a plurality of candidate nucleotide sequences, the score being obtained in a calculation using the probabilistic spectrum and upon at least one reference nucleotide sequence H, the score being indicative of the candidate nucleotide sequence being a variant of H and furthermore being indicative of the probability that the candidate would give rise to the hybridization signal  $I(\bar{x})$ ; and
- (c) selecting one or more candidate nucleotide sequences having an essentially maximal score.

Claim 64 (amended) A computer program product comprising a computer useable medium having computer readable program code embodied therein for obtaining a candidate nucleotide sequence, the candidate nucleotide sequence being indicative of a sequence of a target polynucleotide molecule T, T producing a hybridization signal  $I(\bar{x})$  upon incubating T with a polynucleotide  $\bar{x}$  for each polynucleotide  $\bar{x}$  in a set E of polynucleotides, the computer program product comprising:

- (a) for each polynucleotide  $\bar{x}$  in the set E of polynucleotides, computer readable program code for causing the computer to obtain a probability  $P_0(\bar{x})$  of  $I(\bar{x})$  the sequence  $\bar{x}$  is not

complementary to a subsequence of T and a probability  $P_1(\bar{x})$  of  $I(\bar{x})$  when the sequence  $\bar{x}$  is complementary to a subsequence of T;

- (b) computer readable program code for causing the computer to assign a score to each of a plurality of candidate nucleotide sequences, the score obtained in a calculation using the probabilistic spectrum and at least one reference nucleotide sequence H, the score being indicative of the candidate nucleotide sequence being a variant of H and furthermore being indicative of the probability that the candidate would give rise to the hybridization signal  $I(\bar{x})$ ; and
- (c) computer readable program code for causing the computer to select a candidate nucleotide sequence having an essentially maximal score.

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